

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: SANOFI
 (B) STREET: 32,34 rue MARBEUF
 (C) CITY: PARIS
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE (ZIP): 75374
 (G) TELEPHONE: 0153774000
 (H) TELEFAX: 0153774133

(ii) TITLE OF INVENTION: IL-13 receptor

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: Carcinoma
 (G) CELL TYPE: renal
 (H) CELL LINE: caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTGCCTGTC GCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AAATGGCTTA	60
ATTCGTTTGC TTGGCTATCG GATGCTTATA TACCTTTCTG ATAAGCACAA CATTTGGCTG	120
TACAAGCTTT TGCAC TTCAT CTT CAGACAC CGAGATAAAA GTTAACCCTC CTCAGGATTT	180
TGAGATAGTG GATTATGAAG AGAACCCGGA TACTTAGGTT ATCTCTATTT GCAATGGCAA	240
CCCCCACTGT CTCTGGATCA TTTGTGTTG TGAAAGGAAT GCACAGTGGA ATATGAAC TA	300
AAATACCGAA ACATTGGTAG TGAAACATGG AAGGCTAGTG TAGAGGTTAC CATCATTACT	360
AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAATT ATAGAAGGGC	420
GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCAA	480
TTGCTAGGAG TGGGCAGAAA CTACTTATTG GATATCACCA CAAGGAATTC CAGAACTAA	540
AGTTCAGGAT TAAGTTTTTG GTAGAATGGA TTGCGTATAT TACAATTGGC AATATTTACT	600
CTGTTCTTGG AAACCTGGCA TAGGTTACAT TATGTCTGGG TACTTCTTGA TACCAATTAC	660
AACTTGTTTT ACTGGTATGA GGGCTTGGAT CATGCATTAA ATATATTTGG AAACAGTGTG	720
TTGATTACAT CAAGGCTGAT GGACAAAATA TAGGATGCAG ATTTCCCTAT TTGGCAATAA	780

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AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATTT GTGTTAATGG ATCATCAGAG 840
 AACAAGCCTG AAATATCAAG GAATCAGATC CAGTTATTTT ACTTTTCAGC TTCAAAATAT 900
 AGTTAAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG 960
 TGAAATTAAG CTGAAATGGA GCATACCTTT GTTTAGGCGT GGACCTATTC CAGCAAGGTG 1020
 TTTTGATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTTTG 1080
 GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA 1140
 ATAGAGTTTT TAGTAGCAAT TATGCTTTGT AGTAAGAAGC AAAGTGAATA TTTATTGCTC 1200
 AGATGACGGA ATTTGGGCAA AGAATCAAGT AGTGAGTGGG GTGATAAACA ATGCTGGGAA 1260
 GGTGAAGACC TATCGAAGAA AACTTTGCTA GTAGCTGGGA TCGTTTCTGG CTACCATTG 1320
 GTTTCATCTT AATATTAGTT ATATTTGTAA CCGGTCTGCT TAGTGAATGT TGCCTAAGCC 1380
 AAACACCTAC CCAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTGCATC 1440
 TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA 1500
 TATGAGTCTC AATAAACTGA ATTTTCTTGT CGAATGTTG 1539

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
 - (G) CELL TYPE: renal
 - (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
 1 5 10 15
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45
 Leu Tyr Leu Gln Trp Gln Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125

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Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: RENAL
- (H) CELL LINE: Caki-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAGCCCGGC	CGGGCTCCGA	GGCGAGAGGC	TGCATGGAGT	GGCCGGCGCG	GCTCTGCGGG	60
CTGTGGGCGC	TGCTGCTCTG	CGCCGGCGGC	GGGGGCGGGG	GCGGGGCGCG	CGCGCCTACG	120
GAAACTCAGC	CACCTGTGAC	AAATTTGAGT	GTCTCTGTTG	AAAACCTCTG	CACAGTAATA	180
TGGACATGGA	ATCCACCCGA	GGGAGCCAGC	TCAAATTGTA	GTCTATGGTA	TTTTAGTCAT	240
TTTGGCGACA	AACAAGATAA	GAAAATAGCT	CCGGAAACTC	GTGTTCAAT	AGAAGTACCC	300
CTGAATGAGA	GGATTTGTCT	GCAAGTGGGG	TCCAGTGTA	GCACCAATGA	GAGTGAGAAG	360
CCTAGCATTT	TGGTTGAAAA	ATGCATCTCA	CCCCCAGAAG	GTGATCCTGA	GTCTGCTGTG	420
ACTGAGCTTC	AATGCATTTG	GCACAACCTG	AGCTACATGA	AGTGTTCCTG	GCTCCCTGGA	480
AGGAATACCA	GTCCCGACAC	TAATACTACT	CTCTACTATT	GGCACAGAAG	CCTGGAAAAA	540
ATTCATCAAT	GTGAAAACAT	CTTTAGAGAA	GGCCAATACT	TTGGTTGTTC	CTTTGATCTG	600
ACCAAAGTGA	AGGATTCCAG	TTTTGAACAA	CACAGTGTC	AAATAATGGT	CAAGGATAAT	660
GCAGGAAAAA	TTAAACCATC	CTTCAATATA	GTGCCTTTAA	CTTCCCGTGT	GAAACCTGAT	720
CCTCCACATA	TTAAAAACCT	CTCCTTCCAC	AATGATGACC	TATATGTGCA	ATGGGAGAAT	780
CCACAGAATT	TTATTAGCAG	ATGCCTATTT	TATGAAGTAG	AAGTCAATAA	CAGCCAAACT	840
GAGACACATA	ATGTTTTCTA	CGTCCAAGAG	GCTAAATGTG	AGAATCCAGA	ATTTGAGAGA	900
AATGTGGAGA	ATACATCTTG	TTTCATGGTC	CCTGGTGTTT	TTCCTGATAC	TTTGAACACA	960
GTCAGAATAA	GAGTCAAAAC	AAATAAGTTA	TGCTATGAGG	ATGACAAACT	CTGGAGTAAT	1020
TGGAGCCAAG	AAATGAGTAT	AGGTAAGAAG	CGCAATTCCA	CACTCTACAT	AACCATGTTA	1080
CTCATTGTTT	CAGTCATCGT	CGCAGGTGCA	ATCATAGTAC	TCCTGCTTTA	CCTAAAAAGG	1140
CTCAAGATTA	TTATATTCCC	TCCAATTCCCT	GATCCTGGCA	AGATTTTTAA	AGAAATGTTT	1200
GGAGACCAGA	ATGATGATAC	TCTGCACTGG	AAGAAGTACG	ACATCTATGA	GAAGCAAACC	1260
AAGGAGGAAA	CCGACTCTGT	AGTGCTGATA	GAAAACCTGA	AGAAAGCCTC	TCAGTGATGG	1320
AGATAATTTA	TTTTTACCTT	CACTGTGACC	TTGAGAAGAT	TCTTCCCATT	CTCCATTGTG	1380
TATCTGGGAA	CTTATTAAAT	GGAAACTGAA	ACTACTGCAC	CATTTAAAAA	CAGGCAGCTC	1440
ATAAGAGCCA	CAGGTCTTTA	TGTTGAGTCG	CGCACCAGAA	AACTAAAAAT	AATGGGCGCT	1500
TTGGAGAAGA	GTGTGGAGTC	ATTCTCATTG	AATTATAAAA	GCCAGCAGGC	TTCAAACCTAG	1560
GGGACAAAGC	AAAAAGTGAT	GATAGTGGTG	GAGTTAATCT	TATCAAGAGT	TGTGACAACCT	1620
TCCTGAGGGA	TCTATACTTG	CTTTGTGTTT	TTTGTGTCAA	CATGAACAAA	TTTTATTTGT	1680
AGGGGAACCT	ATTTGGGGTG	CAAATGCTAA	TGTCAAACCT	GAGTCACAAA	GAACATGTAG	1740
AAAACAAAAT	GGATAAAATC	TGATATGTAT	TGTTTGGGAT	CCTATTGAAC	CATGTTTGTG	1800
GCTATTAAAA	CTCTTTTAAC	AGTCTGGGCT	GGGTCCGGTG	GCTCACGCCT	GTAATCCCAG	1860
CAATTTGGGA	GTCCGAGGCG	GGCGGATCAC	TCGAGGTCAG	GAGTTCCAGA	CCAGCCTGAC	1920
CAAAATGGTG	AAACCTCCTC	TCTACTAAAA	CTACAAAAAT	TAAGTGGGTG	TGGTGGCGCG	1980
TGCCTGTAAT	CCCAGCTACT	CGGGAAGCTG	AGGCAGGTGA	ATTGTTTGAA	CCTGGGAGGT	2040

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GGAGGTTGCA GTGAGCAGAG ATCACACCAC TGCACTCTAG CCTGGGTGAC AGAGCAAGAC 2100
TCTGTCTAAA AAACAAAACA AAACAAAACA AAACAAAAAA ACCTCTTAAT ATTCTGGAGT 2160
CATCATTCCC TTCGACAGCA TTTTCCTCTG CTTTGAAAGC CCCAGAAATC AGTGTGGGCC 2220
ATGATGACAA CTACAGAAAA ACCAGAGGCA GCTTCTTTGC CAAGACCTTT CAAAGCCATT 2280
TTAGGCTGTT AGGGGCAGTG GAGGTAGAAT GACTCCTTGG GTATTAGAGT TTCAACCATG 2340
AAGTCTCTAA CAATGTATTT TCTTCACCTC TGCTACTCAA GTAGCATTTA CTGTGTCTTT 2400
GGTTTGTGCT AGGCCCCCGG GTGTGAAGCA CAGACCCCTT CCAGGGGTTT ACAGTCTATT 2460
TGAGACTCCT CAGTTCTTGC CACTTTTTTTT TTTAATCTCC ACCAGTCATT TTTCAGACCT 2520
TTTAACTCCT CAATTCCAAC ACTGATTTCC CCTTTTGCAT TCTCCCTCCT TCCCTTCCTT 2580
GTAGCCTTTT GACTTTTCATT GGAAATTAGG ATGTAAATCT GCTCAGGAGA CCTGGAGGAG 2640
CAGAGGATAA TTAGCATCTC AGGTTAAGTG TGAGTAATCT GAGAAACAAT GACTAATTCT 2700
TGCATATTTT GTAACCTCCA TGTGAGGGTT TTCAGCATTG ATATTTGTGC ATTTTCTAAA 2760
CAGAGATGAG GTGGTATCTT CACGTAGAAC ATTGGTATTC GCTTGAGAAA AAAAGAATAG 2820
TTGAACCTAT TTCTCTTTCT TTACAAGATG GGTCCAGGAT TCCTCTTTTC TCTGCCATAA 2880
ATGATTAATT AAATAGCTTT TGTGTCTTAC ATTGGTAGCC AGCCAGCCAA GGCTCTGTTT 2940
ATGCTTTTGG GGGGCATATA TTGGGTTCCTA TTCTCACCTA TCCACACAAC ATATCCGTAT 3000
ATATCCCCTC TACTCTTACT TCCCCCAAAT TTAAAGAAGT ATGGGAAATG AGAGGCATTT 3060
CCCCCACCCC ATTTCTCTCC TCACACACAG ACTCATATTA CTGGTAGGAA CTTGAGAACT 3120
TTATTTCCAA GTTGTTCAAA CATTTACCAA TCATATTAAT ACAATGATGC TATTTGCAAT 3180
TCCTGCTCCT AGGGGAGGGG AGATAAGAAA CCCTCACTCT CTACAGGTTT GGGTACAAGT 3240
GGCAACCTGC TTCCATGGCC GTGTAGAAGC ATGGTGCCCT GGCTTCTCTG AGGAAGCTGG 3300
GGTTCATGAC AATGGCAGAT GTAAAGTTAT TCTTGAAGTC AGATTGAGGC TGGGAGACAG 3360
CCGTAGTAGA TGTCTACTT TGTCTGCTG TTCTCTAGAA AGAATATTG GTTTTCCTGT 3420
ATAGGAATGA GATTAATTCC TTTCCAGGTA TTTTATAATT CTGGGAAGCA AAACCCATGC 3480
CTCCCCCTAG CCATTTTAC TGTATCCTA TTTAGATGGC CATGAAGAGG ATGCTGTGAA 3540
ATTCCCAACA AACATTGATG CTGACAGTCA TGCAGTCTGG GAGTGGGAA GTGATCTTTT 3600
GTTCCCATCC TCTTCTTTTA GCAGTAAAAT AGCTGAGGGA AAAGGGAGGG AAAAGGAAGT 3660
TATGGGAATA CCTGTGGTGG TTGTGATCCC TAGGTCTTGG GAGCTCTTGG AGGTGTCTGT 3720
ATCAGTGGAT TTCCCATCCC CTGTGGGAAA TTAGTAGGCT CATTTACTGT TTTAGGTCTA 3780
GCCTATGTGG ATTTTTTCTT AACATACCTA AGCAAACCCA GTGTCAGGAT GGTAATTCTT 3840
ATTCTTTCGT TCAGTTAAGT TTTTCCCTTC ATCTGGGCAC TGAAGGATA TGTGAAACAA 3900
TGTTAACATT TTTGGTAGTC TTCAACCAGG GATTGTTTCT GTTTAACTTC TTATAGGAAA 3960
GCTTGAGTAA AATAAATATT GTCTTTTTGT ATGTCACCCA AAAAAAAAAA 4009

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: Carcinoma
 (G) CELL TYPE: renal
 (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Glu	Trp	Pro	Ala	Arg	Leu	Cys	Gly	Leu	Trp	Ala	Leu	Leu	Leu	Cys	1	5	10	15
Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Thr	Glu	Thr	Gln	20	25	30	
Pro	Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	35	40	45	
Ile	Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	50	55	60	
Trp	Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	65	70	75	80
Glu	Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	85	90	95	
Gln	Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	100	105	110	
Leu	Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	115	120	125	
Val	Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	130	135	140	
Ser	Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	145	150	155	160
Tyr	Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	165	170	175	
Phe	Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	180	185	190	
Lys	Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	195	200	205	
Asn	Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	210	215	220	
Arg	Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn	225	230	235	240
Asp	Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	245	250	255	
Cys	Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	260	265	270	
Asn	Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	275	280	285	

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Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
 290 295 300
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
 305 310 315 320
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
 325 330 335
 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
 340 345 350
 Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys
 355 360 365
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
 370 375 380
 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
 385 390 395 400
 Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
 405 410 415
 Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

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